



Research Tools	Reviews	Journal Collection	News & Comment	Books & Labware	Science Jobs	Web Links	
research.bmn.com	Latest Updates	MEDLINE	Swiss Prot	Technical Tips	Structures Database	Mouse Knockout	Section Search

My BMN	Exit
Feedback	Help

MEDLINE

Search

[Browse by Journal](#)

[Browse MESH](#)

[Preferences](#)

[About MEDLINE](#)

Quick Site Search

BioMedNet

[Advanced site search](#)

Medline

[Simple](#) | [Advanced](#) | [Citation](#) | [History](#) | [Results](#) | [Record](#)

Soluble receptors in human disease.

Heaney ML, Golde DW
J Leukoc Biol 1998 Aug 64:135-46

BROWSE : [J Leukoc Biol](#) • [Volume 64](#) • [Issue 2](#)

VIEW : [MEDLINE](#), [full MEDLINE](#), [related records](#)

Abstract

Soluble cytokine receptors naturally arise from genes encoding membrane-bound receptors or are direct derivatives of the receptors themselves. There is mounting evidence that soluble receptors play important roles in human disease states. In many cases, soluble receptors appear to play an integral part in the dynamic interaction between ligands and their membrane-bound receptors in maintaining and restoring health after a pathological insult but, in some instances, dysregulated expression of soluble receptors can contribute to disease pathology. Nonetheless, an appreciation of the biological actions of soluble receptors, particularly as cytokine inhibitors, has led to their therapeutic use in human diseases. Although early clinical trials of soluble receptors have had unexpected toxicities, their application in medicine continues to advance and it is likely that soluble receptors will join hormones, cytokines, and growth factors as established biological therapies.

MeSH

[Extracellular Space](#); [Human](#); [Immunologic Diseases](#); [Receptors, Cytokine](#); [Solubility](#); [Support, U.S. Gov't, P.H.S.](#)

Author Address

Department of Medicine, Memorial Sloan-Kettering Cancer Center, New York, NY 10021, USA. m-heaney@ski.mskcc.org

Order Document

-continued

Thr	Leu	Cys	Thr	Glu	Leu	Thr	Val	Thr	Asp	Ile	Phe	Ala	Ala	Ser	
				50					55					60	
AAG	AAC	ACA	ACT	GAG	AAG	GAA	ACC	TTC	TGC	AGG	GCT	GCG	ACT	GTG	225
Lys	Asn	Thr	Thr	Glu	Lys	Glu	Thr	Phe	Cys	Arg	Ala	Ala	Thr	Val	
				65					70					75	
CTC	CGG	CAG	TTC	TAC	AGC	CAC	CAT	GAG	AAG	GAC	ACT	CGC	TGC	CTG	270
Leu	Arg	Gln	Phe	Tyr	Ser	His	His	Glu	Lys	Asp	Thr	Arg	Cys	Leu	
				80					85					90	
GGT	GCG	ACT	GCA	CAG	CAG	TTC	CAC	AGG	CAC	AAG	CAG	CTG	ATC	CGA	315
Gly	Ala	Thr	Ala	Gln	Gln	Phe	His	Arg	His	Lys	Gln	Leu	Ile	Arg	
				95					100					105	
TTC	CTG	AAA	CGG	CTC	GAC	AGG	AAC	CTC	TGG	GGC	CTG	GCG	GGC	TTG	360
Phe	Leu	Lys	Arg	Leu	Asp	Arg	Asn	Leu	Trp	Gly	Leu	Ala	Gly	Leu	
				110					115					120	
AAT	TCC	TGT	CCT	GTG	AAG	GAA	GCC	AAC	CAG	AGT	ACG	TTG	GAA	AAC	405
Asn	Ser	Cys	Pro	Val	Lys	Glu	Ala	Asn	Gln	Ser	Thr	Leu	Glu	Asn	
				125					130					135	
TTC	TTG	GAA	AGG	CTA	AAG	ACG	ATC	ATG	GAA	GAG	AAA	TAT	TCA	AAG	450
Phe	Leu	Glu	Arg	Leu	Lys	Thr	Ile	Met	Glu	Glu	Lys	Tyr	Ser	Lys	
				140					145					150	
TGT	TCG	AGC	TAG												462
Cys	Ser	Ser	End												
				153											

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (A) DESCRIPTION: hIL-4/R121F

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ATG	GGT	CTC	ACC	TCC	GAA	CTG	CTT	CCC	CCT	CTG	TTC	TTC	CTG	CTA	45
Met	Gly	Leu	Thr	Ser	Gln	Leu	Leu	Pro	Pro	Leu	Phe	Phe	Leu	Leu	
1				5				10						15	
GCA	TGT	GCC	GGC	AAC	TTT	GTC	CAC	GGA	CAC	AAG	TGC	GAT	ATC	ACC	90
Ala	Cys	Ala	Gly	Asn	Phe	Val	His	Gly	His	Lys	Cys	Asp	Ile	Thr	
				20				25						30	
TTA	CAG	GAG	ATC	ATC	AAA	ACT	TTG	AAC	AGC	CTC	ACA	GAG	CAG	AAG	135
Leu	Gln	Glu	Ile	Ile	Lys	Thr	Leu	Asn	Ser	Leu	Thr	Glu	Gln	Lys	
				35				40						45	
ACT	CTG	TGC	ACC	GAG	TTG	ACC	GTA	ACA	GAC	ATC	TTT	GCT	GCC	TCC	180
Thr	Leu	Cys	Thr	Glu	Leu	Thr	Val	Thr	Asp	Ile	Phe	Ala	Ala	Ser	
				50				55						60	
AAG	AAC	ACA	ACT	GAG	AAG	GAA	ACC	TTC	TGC	AGG	GCT	GCG	ACT	GTG	225
Lys	Asn	Thr	Thr	Glu	Lys	Glu	Thr	Phe	Cys	Arg	Ala	Ala	Thr	Val	
				65				70						75	
CTC	CGG	CAG	TTC	TAC	AGC	CAC	CAT	GAG	AAG	GAC	ACT	CGC	TGC	CTG	270
Leu	Arg	Gln	Phe	Tyr	Ser	His	His	Glu	Lys	Asp	Thr	Arg	Cys	Leu	
				80				85						90	
GGT	GCG	ACT	GCA	CAG	CAG	TTC	CAC	AGG	CAC	AAG	CAG	CTG	ATC	CGA	315
Gly	Ala	Thr	Ala	Gln	Gln	Phe	His	Arg	His	Lys	Gln	Leu	Ile	Arg	
				95				100						105	
TTC	CTG	AAA	CGG	CTC	GAC	AGG	AAC	CTC	TGG	GGC	CTG	GCG	GGC	TTG	360
Phe	Leu	Lys	Arg	Leu	Asp	Arg	Asn	Leu	Trp	Gly	Leu	Ala	Gly	Leu	
				110				115						120	